SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: AMGEN INC.
- (ii) TITLE OF INVENTION: TRUNCATED SOLUBLE TUMOR NECROSIS FACTOR
 TYPE-I AND TYPE-II RECEPTORS
- (iii) NUMBER OF SEQUENCES: 81
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: AMGEN INC.
 - (B) STREET: 1840 De Havilland Drive
 - (C) CITY: Thousand Oaks
 - (D) STATE: California
 - (E) COUNTRY: US
 - (F) ZIP: 91320-1789
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/021,443
 - (B) FILING DATE: 09-JUL-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/032,534
 - (B) FILING DATE: 06-DEC-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/037,737
 - (B) FILING DATE: 23-JAN-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/039,314
 - (B) FILING DATE: 07-FEB-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/039,792
 - (B) FILING DATE: 04-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Zindrick, Thomas D.
 - (B) REGISTRATION NUMBER: 32,185
 - (C) REFERENCE/DOCKET NUMBER: A-415E

- 150 -

(2) INFORMATION FOR SEQ ID NO:1:

(i)	SECTIONS	CHARACTERISTICS:
(+ /	SECUENCE	CHARACTERISTICS.

- (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	(X1) SE(JOENG	JE DE	SCRI	PTIC)N: 3	SEQ .	א עו):1:			
					CAA Gln								48
					TGC Cys								96
					GAT Asp								144
					AAC Asn								192
					GGT Gly 70								240
					GGC Gly								288
					CAG Gln								336
					TGC Cys								384
					CTA Leu								432
					GAG Glu 150								480
AAT Asn													483

- 151 -(2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 161 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys

Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser

Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys

Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp

Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp

Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly

Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys 120

His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn

Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu 150

Asn

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 4..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
CAT ATG GAC AGC GTT TGC CCC CAA GGA AAA TAC ATC CAC CCT CAA AAT Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn 1 5 10 15	48
AAT TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn 20 25 30	96
GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser 35 40 45	144
GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys 50 55 60	192
TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr 65 70 75	240
GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His 80 85 90 95	288
TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC TGC TGA TAGGATCC Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Cys * 100 105	332
(2) INFORMATION FOR SEQ ID NO:4:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 107 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn 1 5 10 15	
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp 20 25 30	
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly 35 40 45	
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser 50 55 60	
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val 65 70 75 80	

- 153 -

Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Cys * 100 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 4..333 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: CAT ATG GAC AGC GTT TGC CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn AAT TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT 96 Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn 20 GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC 144 Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC 192 Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys 240 TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT 288 Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His 80

TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC TCT CTG TAA

Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu *

AAGCTT

105

333

339

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(2)	INF	orma	TION	FOR	SEQ	ID	NO:6	:							
		(i)	(B) LEI) TY!	NGTH PE:		0 am	ino . id		s					
	(ii) .	MOLE	CULE	TYP	E: p	rote	in							
	(:	xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	6:				
Met 1	Asp	Ser	Val	Cys 5	Pro	Gln	Gly	Lys	Tyr 10	Ile	His	Pro	Gln	Asn 15	Asn
Ser	Ile	Cys	Cys 20	Thr	Lys	Cys	His	Lys 25	Gly	Thr	Tyr	Leu	Tyr 30	Asn	Asp
Cys	Pro	Gly 35	Pro	Gly	Gln	Asp	Thr 40	Asp	Cys	Arg	Glu	Cys 45	Glu	Ser	Gly
Ser	Phe 50	Thr	Ala	Ser	Glu	Asn 55	His	Leu	Arg	His	Cys 60	Leu	Ser	Cys	Ser
Lys 65	Cys	Arg	Lys	Glu	Met 70	Gly	Gln	Val	Glu	Ile 75	Ser	Ser	Cys	Thr	Val 80
Asp	Arg	Asp	Thr	Val 85	Cys	Gly	Cys	Arg	Lys 90	Asn	Gln	Tyr	Arg	His 95	Tyr
Trp	Ser	Glu	Asn 100	Leu	Phe	Gln	Cys	Phe 105	Asn	Cys	Ser	Leu	* 110		
(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	10:7	:							
	(i)	() ()	QUENCA) LE B) TY C) ST	ENGTH (PE: (RAND	H: 33 nucl	33 ba leic ESS:	ase p acio unkr	oairs i	3						
	(ii)	MOI	LECUI	E TY	PE:	CDNA	Ą								
	(ix)	(<i>I</i>	ATURE A) NA B) LO	ME/K			324								
	(xi)	SEÇ	QUENC	E DE	SCRI	PTIC	N: S	SEQ I	D NO):7:					

CAT ATG GAC AGC GTT TGC CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT

Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn
1 TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT

Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn
20 25 TAC TGT TGC TGT ASN
30

									100							
GAC Asp	TGT Cys	CCA Pro	GGC Gly 35	CCG Pro	GGG Gly	CAG Gln	GAT Asp	ACG Thr 40	GAC Asp	TGC Cys	AGG Arg	GAG Glu	TGT Cys 45	GAG Glu	AGC Ser	144
														AGC Ser		192
TCC Ser	AAA Lys 65	TGC Cys	CGA Arg	AAG Lys	GAA Glu	ATG Met 70	GGT Gly	CAG Gln	GTG Val	GAG Glu	ATC Ile 75	TCT Ser	TCT Ser	TGC Cys	ACA Thr	240
GTG Val 80	GAC Asp	CGG Arg	GAC Asp	ACC Thr	ĠTG Val 85	TGT Cys	GGT Gly	TGC Cys	AGG Arg	AAG Lys 90	AAC Asn	CAG Gln	TAC Tyr	CGG Arg	CAT His 95	288
								TGC Cys				TAGO	GGAT(CC		333
(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	8:01	:								
		(i) :	(A)	LEI TYI	NGTH PE: a	: 10° amin				5						
	(:	ii) 1	MOLE	CULE	TYP	E: p	rote	in								
	(:	xi) :	SEQUI	ENCE	DES	CRIP'	TION	: SE	QID	NO:	8:					
Met 1		Ser					Gly		Tyr 10	Ile	His	Pro	Gln	Asn 15	Asn	

Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn 15

Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp 20

Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly 45

Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser 55

Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val 65

Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr 95

Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn * 100 105

(2)	INFO	RMAT	CION	FOR	SEQ	ID N	10 : 9 :									
	(i)	(E (C	A) LE 3) TY C) ST	NGTE PE: RANE	i: 28 nucl	5 ba eic SS:	STIC se p acid unkn nown	airs 1	3							
	(ii)	MOI	LECUI	LE TY	PE:	CDNA	A									
	(ix)	(2		ME/F	(EY:		279									
	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	ON: 5	SEQ I	ID NO):9:						
CAT	ATG Met 1	TGT Cys	ACC Thr	AAG Lys	TGC Cys 5	CAC His	AAA Lys	GGA Gly	ACC Thr	TAC Tyr 10	TTG Leu	TAC Tyr	AAT Asn	GAC Asp	TGT Cys 15	48
CCA Pro	GGC Gly	CCG Pro	GGG Gly	CAG Gln 20	GAT Asp	ACG Thr	GAC Asp	TGC Cys	AGG Arg 25	GAG Glu	TGT Cys	GAG Glu	AGC Ser	GGC Gly 30	TCC Ser	96
TTC Phe	ACC Thr	GCT Ala	TCA Ser 35	GAA Glu	AAC Asn	CAC His	CTC Leu	AGA Arg 40	CAC His	TGC Cys	CTC Leu	AGC Ser	TGC Cys 45	TCC Ser	AAA Lys	144
														GTG Val		192
CGG Arg	GAC Asp 65	ACC Thr	GTG Val	TGT Cys	GGC Gly	TGC Cys 70	AGG Arg	AAG Lys	AAC Asn	CAG Gln	TAC Tyr 75	CGG Arg	CAT His	TAT Tyr	TGG Trp	240
									TGC Cys				AAG	CTT		285
(2)	INF	ORMA'	TION	FOR	SEQ	ID I	NO:1	0:								
		(i)	(A (B) LEI) TY:	NGTH PE:	: 92 amin	ERIS' amin o aci	no a id								
	(ii) l	MOLE	CULE	TYP	E: p	rote	in								
	(:	xi)	SEQU	ENCE	DES	CRIP'	TION	: SE	Q ID	NO:	10:					
Met 1		Thr	Lys	Cys 5	His	Lys	Gly	Thr	Tyr 10	Leu	Tyr	Asn	Asp	Cys 15	Pro	
Gly	Pro	Gly	Gln 20	Asp	Thr	Asp	Cys	Arg 25	Glu	Cys	Glu	Ser	Gly 30	Ser	Phe	

Thr	Ala	Ser 35		Asn	His	Leu	Arg 40	His	Cys	Leu	Ser	Cys 45	Ser	Lys	Cys	
Arg	Lys 50	Glu	Met	Gly	Gln	Val 55	Glu	Ile	Ser	Ser	Cys 60	Thr	Val	Asp	Arg	
Asp 65	Thr	Val	Cys	Gly	Cys 70	Arg	Lys	Asn	Gln	Tyr 75	Arg	His	Tyr	Trp	Ser 80	
Glu	Asn	Leu	Phe	Gln 85	Cys	Phe	Asn	Cys	Ser 90	Leu	*					
(2)					SEQ											
	(i	(. (. (.	A) L B) T C) S	ENGT YPE: TRAN	HARAGH: 3: nuc: DEDNI OGY:	15 ba leic ESS:	ase p acio unki	pair: d	S							
	(ii) MO	LECU	LE T	YPE:	CDN	A									
	(ix)	(,		AME/	KEY: ION:		309									
	(xi)	SE	QUEN	CE D	ESCR	IPTIC	on: s	SEQ :	ID N	0:11	:					
CAT					CCT Pro 5											4.8
CAC His	AAA Lys	GGA Gly	ACC Thr	TAC Tyr 20	TTG Leu	TAC Tyr	AAT Asn	GAC Asp	TGT Cys 25	CCA Pro	GGC Gly	CCG Pro	GGG Gly	CAG Gln 30	GAT Asp	9 6
ACG Thr	GAC Asp	TGC Cys	AGG Arg 35	GAG Glu	T GT Cys	GAG Glu	AGC Ser	GGC Gly 40	TCC Ser	TTC Phe	ACC Thr	GCT Ala	TCA Ser 45	GAA Glu	AAC Asn	144
					CTC Leu	Ser										192
CAG Gln	GTG Val 65	GAG Glu	ATC Ile	TCT Ser	TCT Ser	TGC Cys 70	ACA Thr	GTG Val	GAC Asp	CGG Arg	GAC Asp 75	ACC Thr	GTG Val	TGT Cys	GGC ·Gly	240
TGC Cys 80	AGG Arg	AA G Lys	AAC Asn	CAG Gln	TAC Tyr 85	CGG Arg	CAT His	TAT Tyr	TGG Trp	AGT Ser 90	GAA Glu	AAC Asn	CTT Leu	TTC Phe	CAG Gln 95	288
			TGC Cys		CTG Leu	TAA *	AAGC	TT								315

(2)	INFO	RMA:	rion	FOR	SEQ	ID N	NO:12	2:								
	((i) \$	(B)	LEI	CHAP NGTH: PE: &	: 102 amino	2 ami	ino a id		5						
	(i	Li) P	MOLE	CULE	TYPE	E: pı	rote:	in								
	()	(i) \$	SEQUE	ENCE	DESC	CRIPT	rion	: SE	Q ID	NO:	12:					
Met 1	Tyr	Ile	His	Pro 5	Gln	Asn	Asn	Ser	Ile 10	Cys	Суз	Thr	Lys	Cys 15	His	
Lys	Gly	Thr	Tyr 20	Leu	Tyr	Asn	Asp	Cys 25	Pro	Gly	Pro	Gly	Gln 30	Asp	Thr	
Asp	Cys	Arg 35	Glu	Cys	Glu	Ser	Gly 40	Ser	Phe	Thr	Ala	Ser 45	Glu	Asn	His	
Leu	Arg 50	His	Cys	Leu	Ser	Cys 55	Ser	Lys	Cys	Arg	Lys 60	Glu	Met	Gly	Gln	
Val 65	Glu	Ile	Ser	Ser	Cys 70	Thr	Val	Asp	Arg	Asp 75	Thr	Val	Суѕ	Gly	Cys 80	
Arg	Lys	Asn	Gln	Tyr 85	Arg	His	Tyr	Trp	Ser 90	Glu	Asn	Leu	Phe	Gln 95	Cys	
Phe	Asn	Cys	Ser 100	Leu	*											
(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO:1	3:								
	(i)	() ()	QUENCA) LIB) TO	ENGT: YPE : TRAN	H: 25 nucl DEDNI	94 ba leic ESS:	ase p acio unk	pair: d	S							
	(ii)	MO:	LECU	LE T	YPE:	CDN	A									
	(ix)	(.	ATURI A) Ni B) L	AME/												
	(xi)) SE	QUEN	CE D	ESCR:	IPTI	: : NC	SEQ :	ID N	0:13	:					
CAT			ATT Ile													4.8

AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu 20 25 30

96

	-								CTC Leu		1	144
									TCT Ser		1	192
		Asp	 _						TAC Tyr		2	240
					TTC Phe				CTG Leu	TAA * 95	2	288
AAG	CTT										2	294

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Ile Ser Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn 1 10 15

Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser 20 25 30

Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys $35 \hspace{1cm} 40 \hspace{1cm} 45$

Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr 50 55 60

Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His 65 70 . 75 80

Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu * 85 90 95

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Ser Ile Cys

- (2) INFORMATION FOR SEQ ID NO:16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn Asn Ser Ile Cys 1 5

- (2) INFORMATION FOR SEQ ID NO:17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln Asn Asn Ser Ile Cys 1 5

- (2) INFORMATION FOR SEQ ID NO:18:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Gln Asn Asn Ser Ile Cys 1 5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Pro Gln Asn Asn Ser Ile Cys 1

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile His Pro Gln Asn Asn Ser Ile Cys 1

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys 1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:23:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys 1 5 10

- (2) INFORMATION FOR SEQ ID NO:24:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys 1 10

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

(2)	INFOR	RMATION FOR SEQ ID NO:26:							
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown							
	(ii)	MOLECULE TYPE: protein							
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO	:26:						
	Cys 1	Pro Gln Gly Lys Tyr Ile His Pro 5	Gln 10	Asn	Asn	Ser	Ile	Cys 15	
(2)	INFO	RMATION FOR SEQ ID NO:27:							
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown							
	(ii)	MOLECULE TYPE: protein							
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO	:27:						
	Val 1	Cys Pro Gln Gly Lys Tyr Ile His 5	Pro 10	Gln	Asn	Asn	Ser	Ile 15	Cys
(2)	INFO	RMATION FOR SEQ ID NO:28:							
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown							
	(ii)	MOLECULE TYPE: protein							
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO	:28:						
	Ser 1	Val Cys Pro Gln Gly Lys Tyr Ile	His	Pro	Gln	Asn	Asn	Ser 15	Ile

Cys

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser 1 5 10 15

Ile Cys

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Phe Cys Cys Ser

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Phe Cys Cys Ser Leu 1 5

(2)	INFO	RMATIO	N FOR	SEQ :	ID N	0:32	:								
	(i)	(B) '	NCE CH LENGTH TYPE: STRAND TOPOLO	: 6 a amino EDNE:	amino o ac. SS:	o ac: id unkn	ids								
	(ii)	MOLEC	ULE TY	PE:]	prot	ein									
	(xi)	SEQUE	NCE DE	SCRI	PTIO	N: S	EQ I	D NO	:32:						
	Phe 1	Cys C	ys Ser	Leu 5	Cys						•				
(2)	INFO	RMATIO	N FOR	SEQ	ID N	0:33	:								
	(i)	(B) (C)	NCE CH LENGTH TYPE: STRAND TOPOLO	I: 7 amin EDNE	amin o ac SS:	o ac id unkn	ids								
	(ii)	MOLEC	ULE TY	PE:	prot	ein									
	(xi)	SEQUE	NCE DE	ESCRI	PTIC	N: S	EQ I	D NC	:33:						
	Phe 1	Cys C	ys Ser	Leu 5	Cys	Leu	I								
(2)	INFO	RMATIC	N FOR	SEQ	ID N	10:34	:								
	(i)	(B) (C)	NCE CH LENGTH TYPE: STRANI TOPOLO	i: 70 nucl DEDNE	5 ba eic SS:	se p acid unkn	airs 1	3							
	(ii)	MOLEC	CULE T	YPE:	CDNA	7									
	(ix)		JRE: NAME/I LOCATI												
	(xi)	SEQUE	ENCE DI	ESCRI	PTIC	ON: S	SEQ I	ID NO	34	:					
Le	G CCC u Pro 1	GCC CA	AG GTG In Val 5	GCA Ala	TTT Phe	ACA Thr	CCC Pro	TAC Tyr 10	GCC Ala	CCG Pro	GAG Glu	CCC Pro	GGG Gly 15	AGC Ser	48
AC. Th	A TGC r Cys	CGG CT	C AGA eu Arg	GAA Glu	TAC Tyr	TAT Tyr	GAC Asp 25	CAG Gln	ACA Thr	GCT Ala	CAG Gln	ATG Met 30	TGC Cys	TGC Cys	96

AGC Ser	AAG Lys	TGC Cys 35	TCG Ser	CCG Pro	GGC Gly	CAA Gln	CAT His 40	GCA Ala	AAA Lys	GTC Val	TTC Phe	TGT Cys 45	ACC Thr	AAG Lys	ACC Thr	144
TCG Ser	GAC Asp 50	ACC Thr	GTG Val	TGT Cys	GAC Asp	TCC Ser 55	TGT Cys	GAG Glu	GAC Asp	AGC Ser	ACA Thr 60	TAC Tyr	ACC Thr	CAG Gln	CTC Leu	192
TGG Trp 65	AAC Asn	TGG Trp	GTT Val	CCC Pro	GAG Glu 70	TGC Cys	TTG Leu	AGC Ser	TGT Cys	GGC Gly 75	TCC Ser	CGC Arg	TGT Cys	AGC Ser	TCT Ser 80	240
GAC Asp	CAG Gln	GTG Val	GAA Glu	ACT Thr 85	CAA Gln	GCC Ala	TGC Cys	ACT Thr	CGG Arg 90	GAA Glu	CAG Gln	AAC Asn	CGC Arg	ATC Ile 95	TGC Cys	288
ACC Thr	TGC Cys	AGG Arg	CCC Pro 100	GGC Gly	TGG Trp	TAC Tyr	TGC Cys	GCG Ala 105	CTG Leu	AGC Ser	AAG Lys	CAG Gln	GAG Glu 110	GGG Gly	TGC Cys	336
CGG Arg	CTG Leu	TGC Cys 115	GCG Ala	CCG Pro	CTG Leu	CGC Arg	AAG Lys 120	TGC Cys	CGC Arg	CCG Pro	GGC Gly	TTC Phe 125	GGC Gly	GTG Val	GCC Ala	384
AGA Arg	CCA Pro 130	GGA Gly	ACT Thr	GAA Glu	ACA Thr	TCA Ser 135	GAC Asp	GTG Val	GTG Val	TGC Cys	AAG Lys 140	CCC Pro	TGT Cys	GCC Ala	CCG Pro	432
GGG Gly 145	ACG Thr	TTC Phe	TCC Ser	AAC Asn	ACG Thr 150	ACT Thr	TCA Ser	TCC Ser	ACG Thr	GAT Asp 155	ATT	TGC Cys	AGG Arg	CCC Pro	CAC His 160	480
CAG Gln	ATC Ile	TGT Cys	AAC Asn	GTG Val 165	GTG Val	GCC Ala	ATC Ile	CCT Pro	GGG Gly 170	AAT Asn	GCA Ala	AGC Ser	AGG Arg	GAT Asp 175	GCA Ala	528
GTC Val	TGC Cys	A CG Thr	TCC Ser 180	ACG Thr	TCC Ser	CCC Pro	ACC Thr	CGG Arg 185	AGT Ser	ATG Met	GCC Ala	CCA Pro	GGG Gly 190	GCA Ala	GTA Val	576
CAC His	TTA Leu	CCC Pro 195	CAG Gln	CCA Pro	GTG Val	TCC Ser	ACA Thr 200	CGA Arg	TCC Ser	CAA Gln	CAC His	ACG Thr 205	Gln	CCA Pro	ACT Thr	624
CCA Pro	GAA Glu 210	Pro	AGC Ser	ACT Thr	GCT Ala	CCA Pro 215	Ser	ACC Thr	TCC Ser	TTC Phe	CTG Leu 220	Leu	CCA Pro	ATG Met	GGC Gly	672
	Ser				GAA Glu 230	Gly										705

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser 1 5 10 15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys 20 25 30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr 35 40 45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu 50 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser 65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys 85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys 100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala 115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro 130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His 145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala 165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val 180 . 185 . 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr 195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly 210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp 225 230 230

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ala Gln Met Cys

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Thr Ala Gln Met Cys
1 5

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gln Thr Ala Gln Met Cys
1 5

- (2) INFORMATION FOR SEQ ID NO:39:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Asp Gln Thr Ala Gln Met Cys
1 5

- (2) INFORMATION FOR SEQ ID NO:40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Tyr Asp Gln Thr Ala Gln Met Cys 1

- (2) INFORMATION FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Tyr Tyr Asp Gln Thr Ala Gln Met Cys 1

- (2) INFORMATION FOR SEQ ID NO:42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 1 5 10

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys
1 10

- (2) INFORMATION FOR SEQ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 1 5 10

- (2) INFORMATION FOR SEQ ID NO:45:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys
1 10

- (2) INFORMATION FOR SEQ ID NO:46:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

	(ii)	MOLECULE TYPE: protein
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:46:
	Cys 1	Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 5 10
(2)	INFO	RMATION FOR SEQ ID NO:47:
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown
	(ii)	MOLECULE TYPE: protein
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:47:
	Thr 1	Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 5 10 15
(2)	INFO	RMATION FOR SEQ ID NO:48:
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown
	(ii)	MOLECULE TYPE: protein
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:48:
	Ser 1	Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 5 10 15
(2)	INFO	RMATION FOR SEQ ID NO:49:
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met
1 10 15

Cys

- (2) INFORMATION FOR SEQ ID NO:50:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Cys

- (2) INFORMATION FOR SEQ ID NO:51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala 1 5 10 15

Gln Met Cys

- (2) INFORMATION FOR SEQ ID NO:52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr 1 10 15

Ala Gln Met Cys 20

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln 1 5 10 15

Thr Ala Gln Met Cys

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp 1 10 15

Gln Thr Ala Gln Met Cys 20

(2)	INFORMATION	FOR	SEQ	ID	NO:55
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr 1 5 10 15

Asp Gln Thr Ala Gln Met Cys

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr 1 5 10 15

Tyr Asp Gln Thr Ala Gln Met Cys
20

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu
1 10 15

Tyr Tyr Asp Gln Thr Ala Gln Met Cys
20 25

(2)	INFORMATION	FOR	SEQ	ID	NO:58:
-----	-------------	-----	-----	----	--------

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg 1 5 10 15

Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 20 25

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu 1 10 15

Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
1 10 15

Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys
20 25

(2)	INFORMATION	FOR	SEQ	ID	NO:61:
-----	-------------	-----	-----	----	--------

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
1 10 15

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr 1 5 10 15

Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys 25 20

- (2) INFORMATION FOR SEQ ID NO:64:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Pro Leu Arg

- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ala Pro Leu Arg Lys

- (2) INFORMATION FOR SEQ ID NO:66:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ala Pro Leu Arg Lys Cys

(2)	INFORMATION FOR SEQ ID NO:67:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown 	
	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
	Ala Pro Leu Arg Lys Cys Arg 1 5	
(2)	INFORMATION FOR SEQ ID NO:68:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
GGT	TAGCCAT ATGGACAGCG TTTGCCCCCA A	31
(2)	INFORMATION FOR SEQ ID NO:69:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
ccc.	AAGCTTT TACAGAGAGC AATTGAAGCA CTG	33

(2)) INFORMATION FOR SEQ ID NO:70:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO	:70:
ACTC	TCGAGGAT CCGCGGATAA ATAAGTAACG ATCCGGT	CCA 40
(2)) INFORMATION FOR SEQ ID NO:71:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 41 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO	:71:
CAGG	GGTCGGAT CCTATCAGCA GAAGCACTGG AAAAAGGT	TTT C 41
(2)) INFORMATION FOR SEQ ID NO:72:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 31 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO	:72:
GGTI	TTAGCCAT ATGGACAGCG TTTGCGCCCA A	31
(2)) INFORMATION FOR SEQ ID NO:73:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 34 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
CGCGGATCCC TATTAATTGA AGCACTGGAA AAGG	34
(2) INFORMATION FOR SEQ ID NO:74:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
CCCCATATGT ATATCCACCC TCAAAATAAT	30
(2) INFORMATION FOR SEQ ID NO:75:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
CCCAAGCTTT TACAGAGAGC AATTGAAGCA CTG	33
(2) INFORMATION FOR SEQ ID NO:76:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 38 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
CCCCATATGT CGATTAGCTG TACCAAGTGC CACAAAGG	38

(2)) INFO	DRMATION FOR SEQ ID NO:77:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown	
	(ii)	MOLECULE TYPE: cDNA	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:77:	
CCC	CAAGCT	TTT TACAGAGAGC AATTGAAGCA CTG	33
(2)	INFO	DRMATION FOR SEQ ID NO:78:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown	
	(ii)	MOLECULE TYPE: cDNA	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:78:	
CCC	CATAT	GT GTACCAAGTG CCACAAAGGA	30
(2)	INFO	RMATION FOR SEQ ID NO:79:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown	
	(ii)	MOLECULE TYPE: cDNA	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:79:	
CCC	AAGCT	TT TACAGAGAGC AATTGAAGCA CTG	33
(2)	INFO	RMATION FOR SEQ ID NO:80:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown	
	(ii)	MOIECHIE TYPE. ODNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
GGTTAGCCAT ATGGACAGCG TTTGCCCCCA A	31
(2) INFORMATION FOR SEQ ID NO:81:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: unknown(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
CCCAAGCTTT TAGGTGCACA CGGTGTTCTG TTT	33